IN THE CLAIMS:

Please amend claims 1, 2 and 13, cancel claim 39 and add new claim 58.

This listing of claims will replace all prior versions, and listings of the claims in the application.

Listing of the claims

1. **(Currently amended)** A method of identifying a uniquely targeting siRNA nucleotide sequence for a target mRNA sequence of a target species, wherein the siRNA nucleotide sequence lacks complete complementarity to the target mRNA sequence, comprising the steps of:

comparing a database of mRNA sequences from the target species with an siRNA nucleotide sequence that lacks complete complementarity to the target mRNA sequence and that consists of 18-25 nucleotides including at least 11 consecutive nucleotides complementary to the target mRNA sequence to be cleaved by the siRNA nucleotide sequence, wherein the at least 11 consecutive nucleotides complementary to the target mRNA sequence include a nucleotide that is third from an siRNA nucleotide sequence's 5' end; and

determining if, in addition to the target mRNA sequence, one or more additional mRNA sequences in the database are complementary to an 11 consecutive nucleotide sequence of the siRNA nucleotide sequence including the third nucleotide from the 5' end of the siRNA nucleotide sequence,

wherein an absence of one or more additional mRNA sequences in the database that are complementary to an 11 consecutive nucleotide sequence of the siRNA nucleotide sequence including the third nucleotide from the 5' end of the siRNA nucleotide sequence indicates that the siRNA nucleotide sequence is a uniquely targeting siRNA nucleotide sequence that lacks complete complementarity to the target mRNA sequence.

2. **(Currently Amended)** A method of designing a uniquely targeting siRNA for a target mRNA molecule that lacks complete complementarity to the target mRNA sequence comprising the steps of:

a) identifying an siRNA nucleotide sequence for the target mRNA that lacks complete complementarity to the target mRNA sequence, said sequence consisting of 18 25 nucleotides including a nucleotide sequence that has 11 consecutive nucleotides, including the third nucleotide from the siRNA nucleotide sequence's 5' end, that are complementary to an 11 nucleotide sequence that occurs on the target mRNA molecule;

comparing the siRNA nucleotide sequence with a database of mRNA sequences from the target mRNA species; and

determining if, in addition to the target mRNA sequence, one or more additional mRNA sequences in the database are complementary to an 11 consecutive nucleotide sequence of the siRNA nucleotide sequence including the third nucleotide from the 5' end of the siRNA nucleotide sequence,

wherein an absence of one or more additional mRNA sequences in the database that are complementary to an 11 consecutive nucleotide sequence of the siRNA nucleotide sequence including the third nucleotide from the 5' end of the siRNA nucleotide indicates that the of the siRNA nucleotide sequence is a uniquely targeting siRNA nucleotide sequence that lacks complete complementarity to the target mRNA sequence.

3. **(Previously presented)** The method of claim 1 wherein the database of mRNA sequences is a selected from the group consisting of: NCBI database and ENSEMBL database.

4. **(Previously presented)** The method of claim 1 wherein the comparing of the siRNA nucleotide sequence with the database of mRNA sequences from the target mRNA species is performed by a computer.

5. **(Previously presented)** The method of claim 1 wherein the comparing of the siRNA nucleotide sequence with the database of mRNA sequences from the target mRNA species is performed by a computer using a BLAST program.

6-9. **(Canceled)**

10. **(Previously presented)** The method of claim 1 wherein the target mRNA is selected from the group consisting of: an mRNA encoding an oncogene, an mRNA encoding a pathogen protein, a cytokine, a chemokine, a co-stimulatory molecule and a growth factor.

11-12. **(Canceled)**

13 **(Currently amended)** A method of synthesizing a uniquely targeting siRNA for a target mRNA molecule, wherein the siRNA sequence lacks complete complementarity to the target mRNA sequence, comprising the steps of:

identifying ~~or designing~~ a uniquely targeting siRNA nucleotide sequence for the target mRNA that lacks complete complementarity to the target mRNA sequence according to claim 1; and

synthesizing an siRNA molecule having the uniquely targeting siRNA nucleotide sequence.

14-47. **(Canceled)**

48. **(Previously presented)** The method of claim 2 wherein the database of mRNA sequences is a selected from the group consisting of: NCBI database and ENSEMBL database.

49. **(Previously presented)** The method of claim 2 wherein the comparing of the siRNA nucleotide sequence with the database of mRNA sequences from the target mRNA species is performed by a computer.

50. **(Previously presented)** The method of claim 2 wherein the comparing of the siRNA nucleotide sequence with the database of mRNA sequences from the target mRNA species is performed by a computer using a BLAST program.

51. **(Canceled)**.

52. **(Previously presented)** The method of claim 2 wherein the target mRNA is selected from the group consisting of: an mRNA encoding an oncogene, an mRNA encoding a pathogen protein, a cytokine, a chemokine, a co-stimulatory molecule and a growth factor.

53-57. **(Canceled)**.

58. **(New)** A method of synthesizing a uniquely targeting siRNA for a target mRNA molecule, wherein the siRNA sequence lacks complete complementarity to the target mRNA sequence, comprising the steps of:

designing a uniquely targeting siRNA nucleotide sequence for the target mRNA that lacks complete complementarity to the target mRNA sequence according to claim 2; and

synthesizing an siRNA molecule having the uniquely targeting siRNA nucleotide sequence.